2/24	3/24
4/24	5/24
6/24	7/24

Fig.1

```
-60    tgaaaagatagaataaatggcctcgtg

1      ATGGCGCGGCCAGCGCTGCTGGGCGAG
1       M   A   R   P   A   L   L   G   E

61     GGCCAAGTTGCCGCGGCCACAGAAGTT
21      G   Q   V   A   A   A   T   E   V

121    GAAAATCTCTGCACGATAATATGGACG
41      E   N   L   C   T   I   I   W   T

181    ACTCTCAGATATTTTAGTCACTTTGAT
61      T   L   R   Y   F   S   H   F   D

241    CATCGTAAAGAGGAATTACCCCTGGAT
81      H   R   K   E   E   L   P   L   D

301    AGTGCCAATGAAAGTGAGAAGCCTAGC
101     S   A   N   E   S   E   K   P   S

361    GGTGATCCTGAGTCCGCTGTGACTGAG
121     G   D   P   E   S   A   V   T   E

421    AAGTGTTCCTGGCTCCCTGGAAGGAAT
141     K   C   S   W   L   P   G   R   N
```

Fig.1A

ccgaattcggcacgagccgaggcgagggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG
 L   L   V   L   L   L   W   T   A   T   V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC
 Q   P   P   V   T   N   L   S   V   S   V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
 W   S   P   P   E   G   A   S   P   N   C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT
 D   Q   Q   D   K   K   I   A   P   E   T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
 E   K   I   C   L   Q   V   G   S   Q   C

CCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
 P   L   V   K   K   C   I   S   P   P   E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG
 L   K   C   I   W   H   N   L   S   Y   M

ACAAGCCCTGACACACTATACTCTGTACTAT
 T   S   P   D   T   H   Y   T   L   Y   Y

Fig. IB

```
481   TGGTACAGCAGCCTGGACAAAAGTCGT
161    W   Y   S   S   L   E   K   S   R

541   ATTGCTTGTTCCTTTAAATTGACTAAA
181    I   A   C   S   F   K   L   T   K

601   ATAATGGTCAAGGATAATGCTGGGAAA
201    I   M   V   K   D   N   A   G   K

661   TCCTATGTGAAACCTGATCCTCCACAT
221    S   Y   V   K   P   D   P   P   H

721   TTAGTGCAGTGGAAGAATCCACAAAAT
241    L   V   Q   W   K   N   P   Q   N

781   GTCAATAATACTCAAACCGACCGACAT
261    V   N   N   T   Q   T   D   R   H

841   AATTCCGAATCTGATAGAAACATGGAG
281    N   S   E   S   D   R   N   M   E

901   GCCGACGCTGTCTACACAGTCAGAGTA
301    A   D   A   V   Y   T   V   R   V

961   AACAAACTGTGGAGTGATTGGAGTGAA
321    N   K   L   W   S   D   W   S   E
```

Fig. lC

```
CAATGTGAAAACATCTATAGAGAAGGTCAACAC
 Q   C   E   N   I   Y   R   E   G   Q   H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
 V   E   P   S   F   E   H   Q   N   V   Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
 I   R   P   S   C   K   I   V   S   L   T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
 I   K   H   L   L   L   K   N   G   A   L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
 F   R   S   R   C   L   T   Y   E   V   E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
 N   I   L   E   V   E   E   D   K   C   Q

GGTACAAGTTGTTTCCAACTCCCTGGTGTTCTT
 G   T   S   C   F   Q   L   P   G   V   L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
 R   V   K   T   N   K   L   C   F   D   D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
 A   Q   S   I   G   K   E   Q   N   S   T
```

Fig. ID

```
1021    TTCTACACCACCATGTTACTCACCATT
341       F   Y   T   T   M   L   L   T   I

1081    CTTTTTTACCTGAAAAGGCTTAAGATC
361       L   F   Y   L   K   R   L   K   I

1141    ATTTTTAAAGAAATGTTTGGAGACCAG
381       I   F   K   E   M   F   G   D   Q

1201    ATCTATGAGAAACAATCCAAAGAAGAA
401       I   Y   E   K   Q   S   K   E   E

1261    AAAGCAGCTCCTTGAtggggagaagtg
421       K   A   A   P   *

1321    gatttattgcattctccatttgttatc
1381    cttgaaaaacaggcagctcctaagagc
1441    ccaaacccaaaggagctccttccaaga
1501    ccctaaaagcagatgttttgccaaatc
1561    accatcaattcatctaatcaggaattg
```

Fig.IE

```
CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
 P   V   F   V   A   V   A   V   I   I   L

ATTATATTTCCTCCAATTCCTGATCCTGGCAAG
 I   I   F   P   P   I   P   D   P   G   K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
 N   D   D   T   L   H   W   K   K   Y   D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
 T   D   S   V   V   L   I   E   N   L   K

atttctttcttgccttcaatgtgaccctgtgaa

tggggacttgttaaatagaaactgaaactact
cacaggtcttgatgtgactttttgcattgaaaac
aaagcaagagttcttctcgttccttgttccaat
cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaggaatctctgcttgctctg
```

Fig. IF

NR4 EXPRESSION IN MOUSE TISSUES
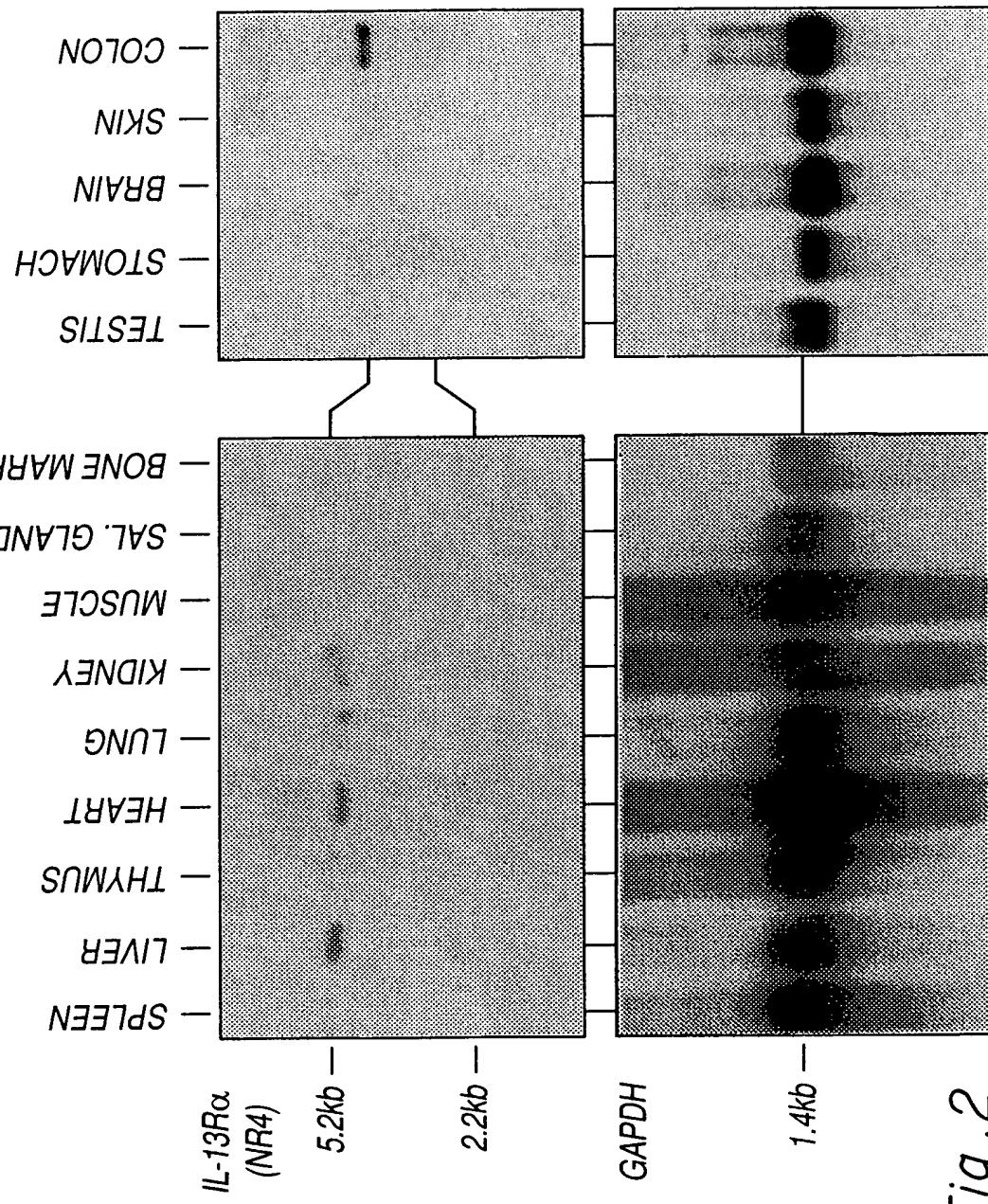
Fig .2
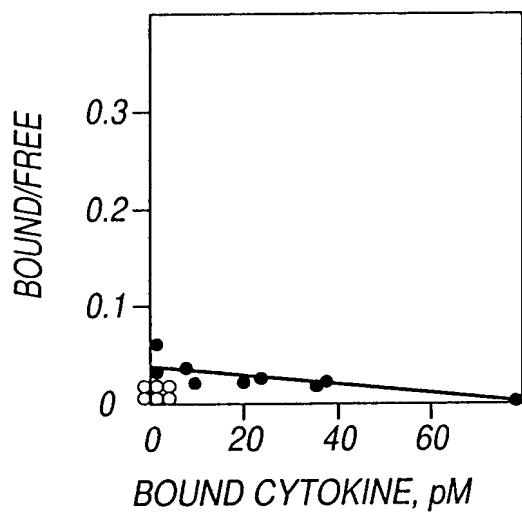
*Fig.3A*
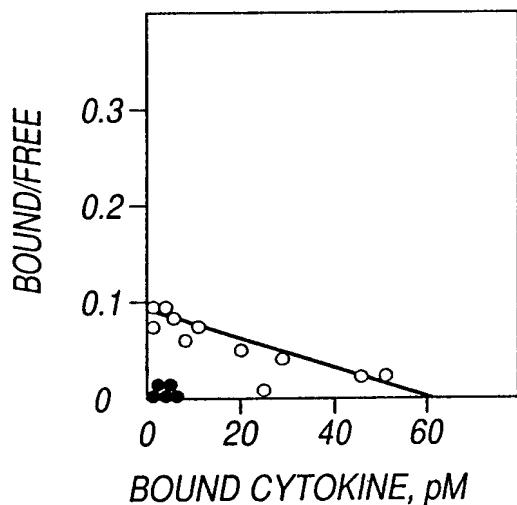
Fig.3B
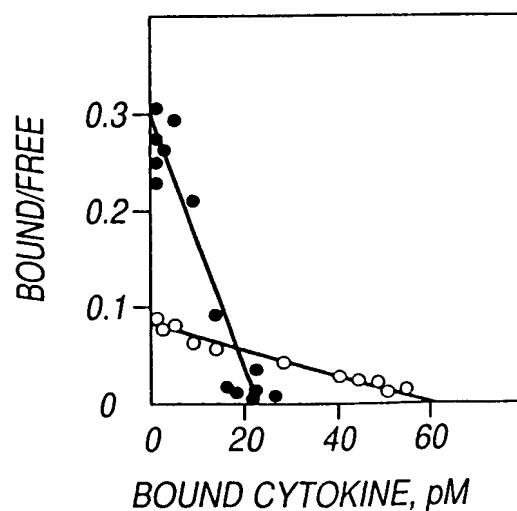
Fig.3C

Fig.4A

Fig.4B

Fig.4C

Fig.4D

VIABLE CELLS, % MAXIMUM NO.

100

50

0

0   0.073   1.17   18.7   300

(CYTOKINE), ng/ml

Fig.5A

VIABLE CELLS, % MAXIMUM NO.

100

50

0

0   0.073   1.17   18.7   300

(CYTOKINE), ng/ml
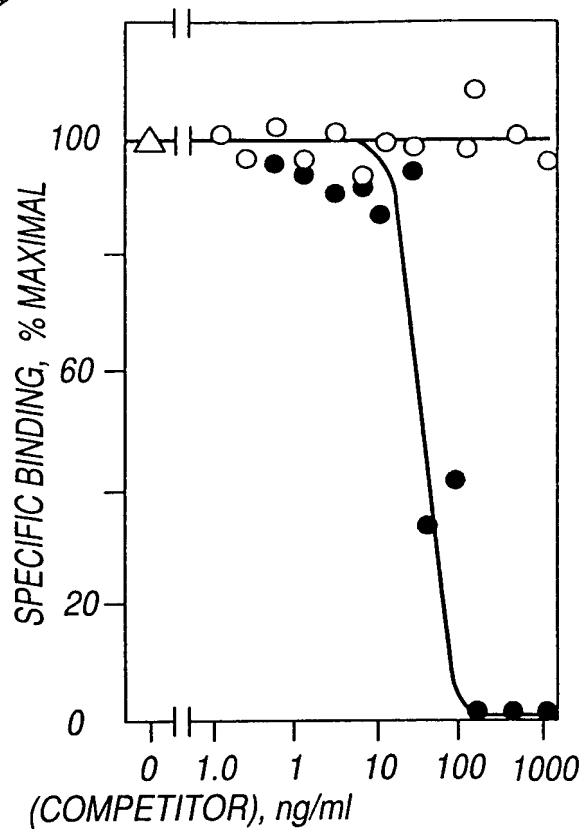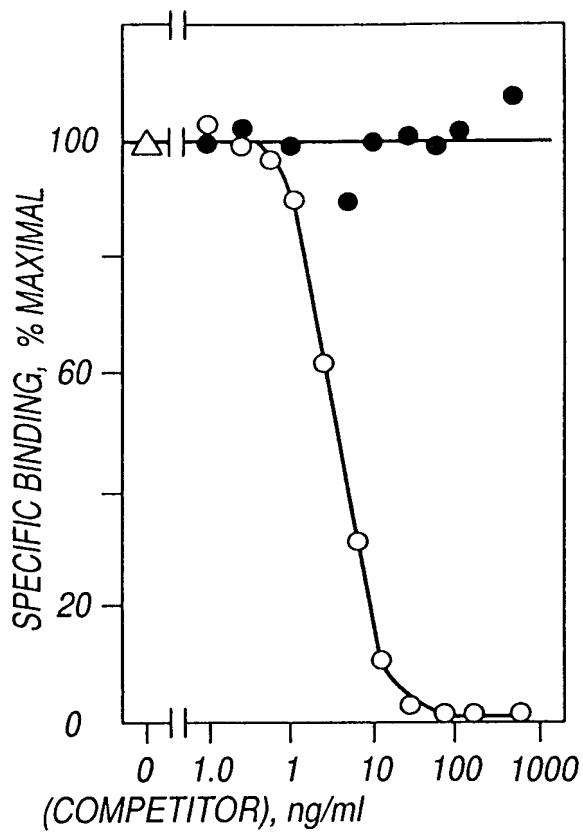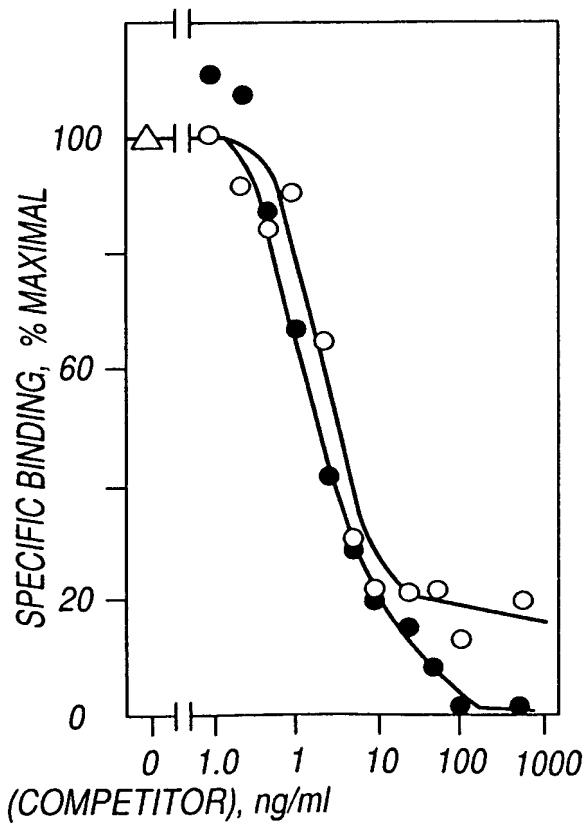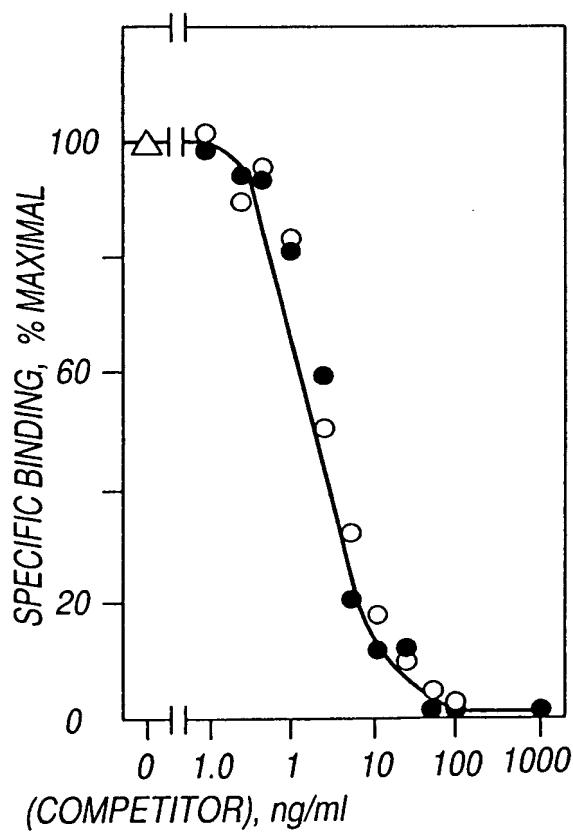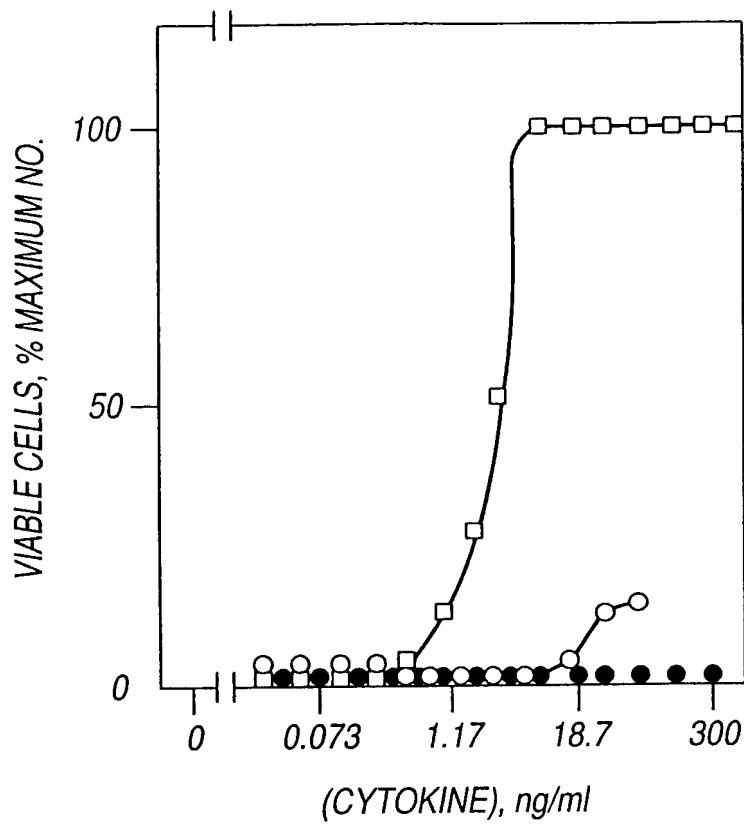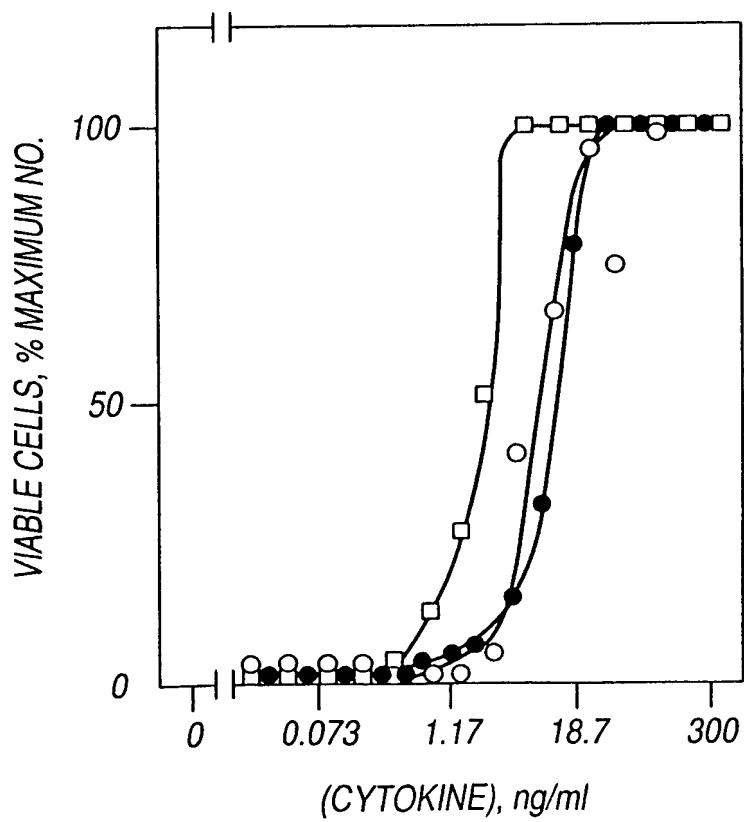
Fig.5B

CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R α)
GENE
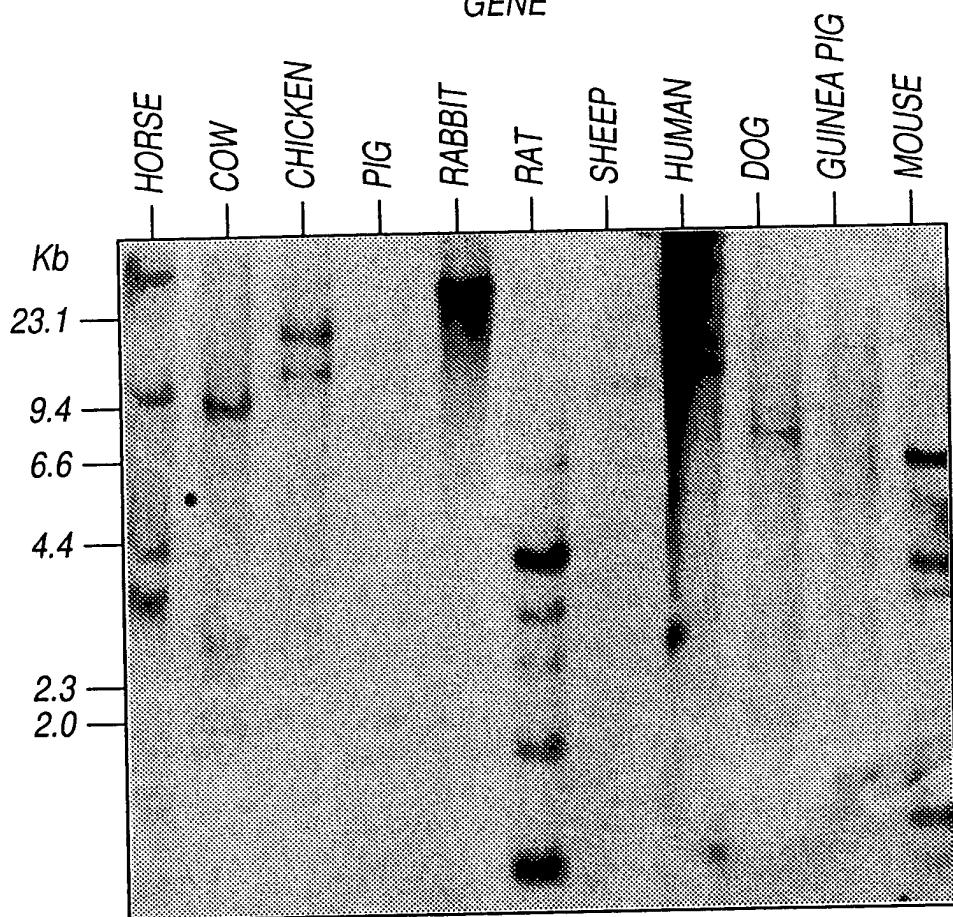
Fig.6

(major)

```
DYKDD  DDYKD  DDESR  TEVQP  PVTXL  SV
1      5      10     15     20     25
```

(minor)

```
ASISS  SDYKD  DDESR  TEVQP  PVTXL  SV
1      5      10     15     20     25
```

Fig.10

14/24	15/24
16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24

Fig.7

H   gagtctaacacggaccaaggagtttaac

M   -60   tgaaaagatagaataaatggcctcgtgc

```
H              M   E   W   P   A   R   L   C   G
               ATGGAGTGGCCGGCGCGGCTCTGCGGGC
               *           *   *       *
M    1         ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M    1          M   A   R   P   A   L   L   G   E


H               G   G   G   G   A   P   T   E   T
H               GGGGGCGGGGGCGCGCCTACGGAAACTC
                *           *       *   *
M    61        GGCCAAGTTGCCGCGGCCACAGAAGTTC
M    21         G   Q   V   A   A   A   T   E   V


H               E   N   L   C   T   V   I   W   T
H               GAAAACCTCTGCACAGTAATATGGACAT
                *   *   *   *   *       *   *   *
M    121       GAAAATCTCTGCACGATAATATGGACGT
M    41         E   N   L   C   T   I   I   W   T


H               S   L   W   Y   F   S   H   F   G
H               AGTCTATGGTATTTTAGTCATTTTGGCG
                    *       *   *   *   *   *
M    181       ACTCTCAGATATTTTAGTCACTTTGATG
M    61         T   L   R   Y   F   S   H   F   D
```

Fig. 7A

```
acgtgcggccggggttccgaggcgagaggctgc
    ....         .......... .  ....
cgaattcggcacgagccgaggcgagggcctgc


L   W   A   L   L   L   C   A   G   G   G   G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC
*           *   *   *
TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---
L   L   V   L   L   L   W   T   A   T   V   -


Q   P   P   V   T   N   L   S   V   S   V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
*   *   *   *   *   *   *   *   *   *   *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q   P   P   V   T   N   L   S   V   S   V


W   N   P   P   E   G   A   S   S   N   C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
*       *   *   *   *   *   *       *   *
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W   S   P   P   E   G   A   S   P   N   C


D   K   Q   D   K   K   I   A   P   E   T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
*       *   *   *   *   *   *   *   *   *
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D   Q   Q   D   K   K   I   A   P   E   T
```

Fig. 7B

```
H              R   R   S   I   E   V   P   L   N
H              CGTCGTTCAATAGAAGTACCCCTGAATG
                  *           *       *   *

M   241        CATCGTAAAGAGGAATTACCCCTGGATG
M    81        H   R   K   E   E   L   P   L   D


H                  S   T   N   E   S   E   K   P   S
H                  AGCACCAATGAGAGTGAGAAGCCTAGCA
                      *       *   *   *   *   *   *   *

M   301        AGTGCCAATGAAAGTGAGAAGCCTAGCC
M   101            S   A   N   E   S   E   K   P   S


H                  G   D   P   E   S   A   V   T   E
H                  GGTGATCCTGAGTCTGCTGTGACTGAAC
                      *   *   *   *   *   *   *   *   *

M   361        GGTGATCCTGAGTCCGCTGTGACTGAGC
M   121            G   D   P   E   S   A   V   T   E


H                  K   C   S   W   L   P   G   R   N
H                  AAGTGTTCTTGGCTCCCTGGAAGGAATA
                      *   *   *   *   *   *   *   *   *

M   421        AAGTGTTCCTGGCTCCCTGGAAGGAATA
M   141            K   C   S   W   L   P   G   R   N


H                  W   H   R   S   L   E   K   I   H
H                  TGGCACAGAAGCCTGGAAAAAATTCATC
```

Fig.7C

```
E    R    I    C    L    Q    V    G    S    Q    C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
*         *    *    *    *    *    *    *    *    *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E    K    I    C    L    Q    V    G    S    Q    C


I    L    V    E    K    C    I    S    P    P    E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
     *    *    *    *    *    *    *    *    *    *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P    L    V    K    K    C    I    S    P    P    E


L    Q    C    I    W    H    N    L    S    Y    M
TTCAATGCATTTGGCACAACCTGAGCTACATG
*         *    *    *    *    *    *    *    *    *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L    K    C    I    W    H    N    L    S    Y    M


T    S    P    D    T    N    Y    T    L    Y    Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
*    *    *    *    *         *    *    *    *    *
CAAGCCCTGACACACTATACTCTGTACTAT
T    S    P    D    T    H    Y    T    L    Y    Y


Q    C    E    N    I    F    R    E    G    Q    Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC
```

Fig.7D

```
                       *                *    *    *    *
M   481   TGGTACAGCAGCCTGGAGAAAAGTCGTC
M   161     W   Y   S   S   L   E   K   S   R


H           F   G   C   S   F   D   L   T   K
H         TTTGGTTGTTCCTTTGATCTGACCAAAG
                         *   *   *       *    *    *
M   541   ATTGCTTGTTCCTTTAAATTGACTAAAG
M   181     I   A   C   S   F   K   L   T   K


H           Q   I   M   V   K   D   N   A   G
H         CAAATAATGGTCAAGGATAATGCAGGAA
                 *   *   *   *   *   *   *   *   *
M   601   CAAATAATGGTCAAGGATAATGCTGGGA
M   201     Q   I   M   V   K   D   N   A   G


H           T   S   R   V   K   P   D   P   P
H         ACTTCCCGTGTGAAACCTGATCCTCCAC
                 *   *       *   *   *   *   *    *
M   661   ACTTCCTATGTGAAACCTGATCCTCCAC
M   221     T   S   Y   V   K   P   D   P   P


H           L   Y   V   Q   W   E   N   P   Q
H         CTATATGTGCAATGGGAGAATCCACAGA
                 *       *   *   *       *    *    *
M   721   TTATTAGTGCAGTGGAAGAATCCACAAA
M   241     L   L   V   Q   W   K   N   P   Q
```

Fig.7E

```
 *     *     *     *     *           *     *     *     *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
 Q     C     E     N     I     Y     R     E     G     Q     H

 V     K     D     S     S     F     E     Q     H     S     V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
 *                       *     *     *                       *
TGGAACCT---AGTTTTGAACATCAGAACG TT
 V     E     P     -     S     F     E     H     Q     N     V

 K     I     K     P     S     F     N     I     V     P     L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
 *     *           *     *                 *     *           *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
 K     I     R     P     S     C     K     I     V     S     L

 H     I     K     N     L     S     F     H     N     D     D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
 *     *     *           *                       *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
 H     I     K     H     L     L     L     K     N     G     A

 N     F     I     S     R     C     L     F     Y     E     V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
 *     *           *     *     *     *           *     *     *
ATTTTAGAAGCAGATGCTTAACTTATGAAGTG
 N     F     R     S     R     C     L     T     Y     E     V
```

Fig.7F

```
H              E   V   N   N   S   Q   T   E   T
H              GAAGTCAATAACAGCCAAACTGAGACAC
               *   *   *   *       *   *
M     781      GAGGTCAATAATACTCAAACCGACCGAC
M     261      E   V   N   N   T   Q   T   D   R


H                  E   N   P   E   F   E   R   N   V
H                  GAGAATCCAGAATTTGAGAGAAATGTGG
                   *       *           *   *
M     841          CAGAATTCCGAATCTGATAGAAACATGG
M     281          Q   N   S   E   S   D   R   N   M


H                  L   P   D   T   L   N   T   V   R
H                  CTTCCTGATACTTTGAACACAGTCAGAA
                   *       *               *   *   *
M     901          CTTGCCGACGCTGTCTACACAGTCAGAG
M     301          L   A   D   A   V   Y   T   V   R


H                  D   D   K   L   W   S   N   W   S
H                  GATGACAAACTCTGGAGTAATTGGAGCC
                   *       *   *   *   *       *   *
M     961          GACAACAAACTGTGGAGTGATTGGAGTG
M     321          D   N   K   L   W   S   D   W   S


H                  T   L   Y   I   T   M   L   L   I
H                  ACACTCTACATAACCATGTTACTCATTG
```

Fig. 7G

```
H   N   V   F   Y   V   Q   E   A   K   C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
*   *               *       *       *   *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H   N   I   L   E   V   E   E   D   K   C

E   N   T   S   C   F   M   V   P   G   V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
*       *   *   *   *           *   *   *
AGGGTACAAGTTGTTTCCAACTCCCTGGTGTT
E   G   T   S   C   F   Q   L   P   G   V

I   R   V   K   T   N   K   L   C   Y   E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
        *   *   *   *   *   *   *   *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V   R   V   K   T   N   K   L   C   F   D

Q   E   M   S   I   G   K   K   R   N   S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
            *   *   *   *           *   *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E   A   Q   S   I   G   K   E   Q   N   S

V   P   V   I   V   A   G   A   I   I   V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA
```

Fig.7H

```
                    *          *          *    *    *    *

M    1021    ACCTTCTACACCACCATGTTACTCACCA
M    341        T    F    Y    T    T    M    L    L    T


H              L    L    L    Y    L    K    R    L    K
H            CTCCTGCTTTACCTAAAAAGGCTCAAGA
                *  *        *    *    *    *    *    *
M    1081    CTCCTTTTTTACCTGAAAAGGCTTAAGA
M    361        L    L    F    Y    L    K    R    L    K


H              K    I    F    K    E    M    F    G    D
H            AAGATTTTTAAAGAAATGTTTGGAGACC
                *    *    *    *    *    *    *    *    *
M    1141    AAGATTTTTAAAGAAATGTTTGGAGACC
M    381        K    I    F    K    E    M    F    G    D


H              D    I    Y    E    K    Q    T    K    E
H            GACATCTATGAGAAGCAAACCAAGGAGG
                *    *    *    *    *    *         *    *
M    1201    GACATCTATGAGAAACAATCCAAAGAAG
M    401        D    I    Y    E    K    Q    S    K    E


H              K    K    A    S    Q    *
H            AAGAAAGCCTCTCAGTGAtggagataat
                *    *    *
M    1261    AAGAAAGCAGCTCCTTGAtggggagaag
M    421        K    K    A    A    P    *
```

Fig.7I

```
      *    *       *    *       *       *
TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I  P  V  F  V  A  V  A  V  I  I


I  I  I  F  P  P  I  P  D  P  G
TTATTATATTCCTCCAATTCCTGATCCTGGC
*  *  *  *  *  *  *  *  *  *  *
TCATTATATTTCCTCCAATTCCTGATCCTGGC
I  I  I  F  P  P  I  P  D  P  G


Q  N  D  D  T  L  H  W  K  K  Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*  *  *  *  *  *  *  *  *  *  *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q  N  D  D  T  L  H  W  K  K  Y


E  T  D  S  V  V  L  I  E  N  L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*  *  *  *  *  *  *  *  *  *  *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E  T  D  S  V  V  L  I  E  N  L


ttattttttaccttcactgtgaccttgagaaga

tgatttctttcttgccttcaatgtgaccctgt
```

Fig.7J

Fig.8

Fig.9